



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,746

DATE: 02/08/2002
TIME: 11:18:39

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02082002\I889746.raw

4 <110> APPLICANT: Ruelle, Jean-Louis
6 <120> TITLE OF INVENTION: Novel Compounds
9 <130> FILE REFERENCE: BM45352
11 <140> CURRENT APPLICATION NUMBER: 09/889,746
C--> 12 <141> CURRENT FILING DATE: 2001-12-31
14 <150> PRIOR APPLICATION NUMBER: 9901368.2
15 <151> PRIOR FILING DATE: 1999-01-22
17 <150> PRIOR APPLICATION NUMBER: 9901944.0
18 <151> PRIOR FILING DATE: 1999-01-28
20 <150> PRIOR APPLICATION NUMBER: 9902086.9
21 <151> PRIOR FILING DATE: 1999-01-29
23 <150> PRIOR APPLICATION NUMBER: 9903417.5
24 <151> PRIOR FILING DATE: 1999-02-15
26 <150> PRIOR APPLICATION NUMBER: 9903535.4
27 <151> PRIOR FILING DATE: 1999-02-16
29 <150> PRIOR APPLICATION NUMBER: PCT/EP00/00428
30 <151> PRIOR FILING DATE: 2000-01-19
32 <160> NUMBER OF SEQ ID NOS: 8
34 <170> SOFTWARE: FastSEQ for Windows Version 4.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 1203
38 <212> TYPE: DNA
39 <213> ORGANISM: Neisseria meningitidis
41 <400> SEQUENCE: 1
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43 cagcagttgt acgctcaacc caatgagtca ttaccaacgg ttgaatttga gcctgtggtt 120
44 attaccattt gtaagagcgg tatggactt gccaatcgta tcacgcaat gccccatacc 180
45 accaaagttt tttatgaaga gcaaattcaa gagcaagcaa caggctctcg acagcttgc 240
46 gatgtatgg cacagctcat tccaagtttggggtaagta gtggcaactac cagtaactttt 300
47 gggcaaacca tgcacggtcg tcaagtgc aa ttttggtaa atggcgtgcc tttgacaggt 360
48 tcgcgagaca tctctagaca gcttaatagt atcaatccca atcaagtggc tagaattgaa 420
49 gtttatcag gagcaaccag tatttatggg tctggagcaa caggcggtt gattaatatc 480
50 gttactaagt ctgatttggaa agaggagcaa tttgaaaccc gcattcggtt acatggtagt 540
51 aaatttatcca gtgaaggatcggtt atcagttatcag gtaggtcaga gtgttagcagg tgcacgcgaa 600
52 aatggtaatg tccttgcacg acttgatgtc gactatcgca ccacaggagg ggcatttgat 660
53 gctaacggta aacgcacatcgc tcctgagcct gcccaaactg ataaagcaaga cagcaaaagc 720
54 ctaagtgtca atacaaatgt tgattggcaa ctggacgaca agcaaaat atcaatctggca 780
55 ttgacgcatt ataacgacaa acaagatacc gattatgcac ctgattatgg taatcgccctt 840
56 gcggttgtt ttggagaaaaa gccttcattt aatgccatca aaggcttac attatcagaa 900
57 cagccaaaaaa ccacccaaag caccttaat atcaactatc atcatgatga tttgtgggt 960
58 aacaccatca ataccaatgc ttattatcgc agagagaaaag gcagattta tcccttgc 1020
59 gccccgtttt cgatcgccaa agccctgcctt atttacaaa gcatgaattt gccatcagcc 1080
60 actttggatg cttataccaa ggctccacaa gctcgccctt atgggggtt acaatccgaa 1140

ENTERED

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61 tcttaaggcag aggtactagg gcgtgtccct aatttgaata agcccaaaag agccctattt 1200
62 taa 1203
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 400
66 <212> TYPE: PRT
67 <213> ORGANISM: Neisseria meningitidis
69 <400> SEQUENCE: 2
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71 1 5 10 15
72 Val Ala Val Thr Gln Gln Leu Tyr Ala Gln Pro Asn Glu Ser Leu Pro
73 20 25 30
74 Thr Val Glu Leu Glu Pro Val Val Ile Thr Ile Asp Lys Ser Gly Met
75 35 40 45
76 Ala Leu Ala Asn Arg Ile Thr Gln Met Pro His Thr Thr Lys Val Ile
77 50 55 60
78 Tyr Glu Glu Gln Ile Gln Glu Gln Ala Thr Gly Ser Arg Gln Leu Ala
79 65 70 75 80
80 Asp Val Met Ala Gln Leu Ile Pro Ser Leu Gly Val Ser Ser Gly Thr
81 85 90 95
82 Thr Ser Asn Phe Gly Gln Thr Met His Gly Arg Gln Val Gln Phe Leu
83 100 105 110
84 Leu Asn Gly Val Pro Leu Thr Gly Ser Arg Asp Ile Ser Arg Gln Leu
85 115 120 125
86 Asn Ser Ile Asn Pro Asn Gln Val Ala Arg Ile Glu Val Leu Ser Gly
87 130 135 140
88 Ala Thr Ser Ile Tyr Gly Ser Gly Ala Thr Gly Gly Leu Ile Asn Ile
89 145 150 155 160
90 Val Thr Lys Ser Asp Leu Glu Glu Gln Phe Glu Thr Arg Ile Gly
91 165 170 175
92 Val His Gly Ser Lys Leu Ser Ser Glu Gly Ile Gly Tyr Gln Val Gly
93 180 185 190
94 Gln Ser Val Ala Gly Val Ser Glu Asn Gly Asn Val Leu Ala Arg Leu
95 195 200 205
96 Asp Val Asp Tyr Arg Thr Thr Gly Gly Ala Phe Asp Ala Asn Gly Lys
97 210 215 220
98 Arg Ile Ala Pro Glu Pro Ala Gln Thr Asp Lys Gln Asp Ser Lys Ser
99 225 230 235 240
100 Leu Ser Val Asn Thr Asn Val Asp Trp Gln Leu Asp Asp Lys Gln Asn
101 245 250 255
102 Ile Asn Leu Ala Leu Thr His Tyr Asn Asp Lys Gln Asp Thr Asp Tyr
103 260 265 270
104 Ala Pro Asp Tyr Gly Asn Arg Leu Ala Val Leu Phe Gly Glu Lys Pro
105 275 280 285
106 Ser Leu Asn Ala Ile Lys Gly Leu Ser Leu Ser Glu Gln Pro Lys Thr
107 290 295 300
108 Thr Lys Ser Thr Phe Asn Ile Asn Tyr His His Asp Asp Leu Trp Gly
109 305 310 315 320
110 Asn Thr Ile Asn Thr Asn Ala Tyr Tyr Arg Arg Glu Lys Gly Arg Phe
111 325 330 335

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112	Tyr	Pro	Phe	Val	Ala	Pro	Phe	Ser	Ile	Ala	Lys	Ala	Leu	Pro	Ile	Leu
113			340					345						350		
114	Gln	Ser	Met	Asn	Leu	Pro	Ser	Ala	Thr	Leu	Asp	Ala	Tyr	Thr	Lys	Ala
115			355					360					365			
116	Pro	Gln	Ala	Arg	Ala	Tyr	Gly	Val	Leu	Gln	Ser	Glu	Ser	Lys	Ala	Glut
117			370					375				380				
118	Val	Leu	Gly	Arg	Val	Pro	Asn	Leu	Asn	Lys	Pro	Lys	Arg	Ala	Leu	Phe
119	385						390			395					400	

121 <210> SEQ ID NO: 3

122 <211> LENGTH: 2409

123 <212> TYPE: DNA

124 <213> ORGANISM: *Neisseria meningitidis*

126 <400> SEQUENCE: 3

127 ttggctcggtt tattttcact caaaccaactg gtgctggcat tgggcttctg cttcggcacy 60
128 cattgcggc cccggccatgc cgttgcggcg gagggaaacgg acaatccgac cgccggagga 120
129 agtgttcgga gcgtgtccga acccatgcag cctgcccggcc tgagcctcg ttcgacactgc 180
130 ctgttttgcga gtaacgaaag cggccaaaccc gaaaaaaccg aatctgccgt caaaggaaagc 240
131 ggccaaggggc ctgtgcccga aaaccacacg cgaattgtcg ccgacaagggt ggaaggggcag 300
132 tcgcagggtca aggtacgcgc ggagggcggc gtcgttgcg aacgcaaccg gacgaccctt 360
133 aatgccgact gggcggattt cggccacccg ggcgacaccg ttaccgtagg cgaccggttc 420
134 gcccctcaac aggacggta cgttgcggg ggcgaaaccc tgacctacaa tctcgagcag 480
135 cagacccggcg aagcgcacaa cgttgcgtt gaaaccgaac aaggcggacg gccggctgcaa 540
136 agcgtcagcc gcaccggcg aatgttgggc gaagggcatt acaaactgac gggaaacccaa 600
137 ttcaacacactt gttccggcg cgttgcggc tggatgtca aggcagcctc tgtcgaagcc 660
138 gatcgggaaa aaggcatagg cgttgcggg caccggccct tctgttgcg cggcgttctt 720
139 attttctaca ccccttggc ggacttcccg ctgtacggca accgcaaaaag cggcctgctt 780
140 gttccctcac tgcgttgcggg ttcggacggc gttcccttt cgttccctta ttatttcaac 840
141 ctggccccca atctcgatgc cacgttgcg cccagcgtga tccggcgaacg cggcgggtc 900
142 ttgcacgggc aggtacgcta cctgcggccg gattatgcg gccagtcga cctgacactgg 960
143 ctggccgcacg acaagaaaag cggcaggaat aaccgcgtatc aggcgaaatg gcagcatcg 1020
144 cagacacattt cccgcacacgt tcaggcgggt gtcgatttca accaagtctc cgacagcggc 1080
145 tactaccgcg acttttacgg caacaaaagaa atcgcggca acgtcaaccc caaccggcgt 1140
146 gtatggctgg attatgcgg cagggcggcg ggcggcagcc tgaatgcggg ccttcgggt 1200
147 ctgaaatacc agacgcgtgc aaacccaaagc ggctacaaag acaaaccgta tgcctgtatg 1260
148 cccgcgcctt. cccgcgatttgcg cccgcggg cccgcggg cccgcggg cccgcggg 1320
149 caatttaccc gttcagcca cggccacccg cccgcggca gtcgttgcgt cgtctatccc 1380
150 gacatcaaattt gggatttcag caacagctgg gttacgtcc gttccaaact cggactgcac 1440
151 gcccacattt acagcctcaa cccgttgcg cccgcggcgt cccgcggcact 1500
152 ctaccatcg tcaacatcg cccgcggcgt accttcgaaac gcaatacgcg gatgttgcgc 1560
153 ggagaagtcc tgcggccatcc cccgcggcgt cccgcggcact 1620
154 caaaacgacc tgcggccatcc tgcggccatcc cccgcggcgt cccgcggcact 1680
155 cgtggaaaacc tctattacgg caacgcacagg attaacaccg caaacagccctt 1740
156 gtgcggaaaacc gtatccgg cccgcggcgt cccgcggcact 1800
157 cagaaattctt acttcaaaaaa cccgcggcgt cccgcggcact 1860
158 cccgcggccatcc tgcggccatcc cccgcggcgt cccgcggcact 1920
159 gacagcggca tccactacaa cccaaacgac aacgcggccg agaactacgc cgtcggtgc 1980
160 agctaccgtc cccgcacccgg cccgcggcgt cccgcggcact 2040
161 aaaatctacc tgcggccatcc tgcggccatcc cccgcggcgt cccgcggcact 2100
162 tccgcacaat qccggccatcc tgcggccatcc cccgcggcgt cccgcggcact 2160

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163 gaagccaaaa aaccgataga ggtgctggcg ggtgcggaat acaaaaagcag ttgcggctgc 2220
 164 tggggcgcgg gcgtgtacgc ccaacgctac gttaccggcg aaaacacaccta caaaaacgct 2280
 165 gtcttttct cacttcagtt gaaagacctc agcagtgtcg gcagaaaaccc cgcagacagg 2340
 166 atggatgtcg ccgttcccg cgatatcccc gcccactctc tttccgcccgg acgcaacaaa 2400
 167 cgccctga 2409
 169 <210> SEQ ID NO: 4
 170 <211> LENGTH: 802
 171 <212> TYPE: PRT
 172 <213> ORGANISM: *Neisseria meningitidis*
 174 <400> SEQUENCE: 4
 175 Met Ala Arg Leu Phe Ser Leu Lys Pro Leu Val Leu Ala Leu Gly Phe
 176 1 5 10 15
 177 Cys Phe Gly Thr His Cys Ala Ala Ala Asp Ala Val Ala Ala Glu Glu
 178 20 25 30
 179 Thr Asp Asn Pro Thr Ala Gly Gly Ser Val Arg Ser Val Ser Glu Pro
 180 35 40 45
 181 Met Gln Pro Ala Gly Leu Ser Leu Gly Ser Thr Cys Leu Phe Cys Ser
 182 50 55 60
 183 Asn Glu Ser Gly Lys Pro Glu Lys Thr Glu Ser Ala Val Lys Gly Ser
 184 65 70 75 80
 185 Gly Glu Gly Pro Val Pro Glu Asn His Thr Arg Ile Val Ala Asp Lys
 186 85 90 95
 187 Val Glu Gly Gln Ser Gln Val Lys Val Arg Ala Glu Gly Val Val
 188 100 105 110
 189 Val Glu Arg Asn Arg Thr Thr Leu Asn Ala Asp Trp Ala Asp Tyr Asp
 190 115 120 125
 191 Gln Ser Gly Asp Thr Val Thr Val Gly Asp Arg Phe Ala Leu Gln Gln
 192 130 135 140
 193 Asp Gly Thr Leu Ile Arg Gly Glu Thr Leu Thr Tyr Asn Leu Glu Gln
 194 145 150 155 160
 195 Gln Thr Gly Glu Ala His Asn Val Arg Met Glu Thr Glu Gln Gly Gly
 196 165 170 175
 197 Arg Arg Leu Gln Ser Val Ser Arg Thr Ala Glu Met Leu Gly Glu Gly
 198 180 185 190
 199 His Tyr Lys Leu Thr Glu Thr Gln Phe Asn Thr Cys Ser Ala Gly Asp
 200 195 200 205
 201 Ala Gly Trp Tyr Val Lys Ala Ala Ser Val Glu Ala Asp Arg Glu Lys
 202 210 215 220
 203 Gly Ile Gly Val Ala Lys His Ala Ala Phe Val Phe Gly Gly Val Pro
 204 225 230 235 240
 205 Ile Phe Tyr Thr Pro Trp Ala Asp Phe Pro Leu Asp Gly Asn Arg Lys
 206 245 250 255
 207 Ser Gly Leu Leu Val Pro Ser Leu Ser Ala Gly Ser Asp Gly Val Ser
 208 260 265 270
 209 Leu Ser Val Pro Tyr Tyr Phe Asn Leu Ala Pro Asn Leu Asp Ala Thr
 210 275 280 285
 211 Phe Ala Pro Ser Val Ile Gly Glu Arg Gly Ala Val Phe Asp Gly Gln
 212 290 295 300
 213 Val Arg Tyr Leu Arg Pro Asp Tyr Ala Gly Gln Ser Asp Leu Thr Trp

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214	305	310	315	320
215	Leu Pro His Asp Lys Lys Ser Gly Arg Asn Asn Arg Tyr Gln Ala Lys			
216	325	330	335	
217	Trp Gln His Arg His Asp Ile Ser Asp Thr Leu Gln Ala Gly Val Asp			
218	340	345	350	
219	Phe Asn Gln Val Ser Asp Ser Gly Tyr Tyr Arg Asp Phe Tyr Gly Asn			
220	355	360	365	
221	Lys Glu Ile Ala Gly Asn Val Asn Leu Asn Arg Arg Val Trp Leu Asp			
222	370	375	380	
223	Tyr Gly Gly Arg Ala Ala Gly Ser Leu Asn Ala Gly Leu Ser Val			
224	385	390	395	400
225	Leu Lys Tyr Gln Thr Leu Ala Asn Gln Ser Gly Tyr Lys Asp Lys Pro			
226	405	410	415	
227	Tyr Ala Leu Met Pro Arg Leu Ser Ala Asp Trp Arg Lys Asn Thr Gly			
228	420	425	430	
229	Arg Ala Gln Ile Gly Val Ser Ala Gln Phe Thr Arg Phe Ser His Asp			
230	435	440	445	
231	Ser Arg Gln Asp Gly Ser Arg Leu Val Val Tyr Pro Asp Ile Lys Trp			
232	450	455	460	
233	Asp Phe Ser Asn Ser Trp Gly Tyr Val Arg Pro Lys Leu Gly Leu His			
234	465	470	475	480
235	Ala Thr Tyr Tyr Ser Leu Asn Arg Phe Gly Ser Gln Glu Ala Arg Arg			
236	485	490	495	
237	Val Ser Arg Thr Leu Pro Ile Val Asn Ile Asp Ser Gly Met Thr Phe			
238	500	505	510	
239	Glu Arg Asn Thr Arg Met Phe Gly Gly Glu Val Leu Gln Thr Leu Glu			
240	515	520	525	
241	Pro Arg Leu Phe Tyr Asn Tyr Ile Pro Ala Lys Ser Gln Asn Asp Leu			
242	530	535	540	
243	Pro Asn Phe Asp Ser Ser Glu Ser Ser Phe Gly Tyr Gly Gln Leu Phe			
244	545	550	555	560
245	Arg Glu Asn Leu Tyr Tyr Gly Asn Asp Arg Ile Asn Thr Ala Asn Ser			
246	565	570	575	
247	Leu Ser Ala Ala Val Gln Ser Arg Ile Leu Asp Gly Ala Thr Gly Ala			
248	580	585	590	
249	Glu Arg Phe Arg Ala Gly Ile Gly Gln Lys Phe Tyr Phe Lys Asn Asp			
250	595	600	605	
251	Ala Val Met Leu Asp Gly Ser Val Gly Lys Lys Pro Arg Ser Arg Ser			
252	610	615	620	
253	Asp Trp Val Ala Phe Ala Ser Ser Gly Ile Gly Ser Arg Phe Ile Leu			
254	625	630	635	640
255	Asp Ser Ser Ile His Tyr Asn Gln Asn Asp Lys Arg Ala Glu Asn Tyr			
256	645	650	655	
257	Ala Val Gly Ala Ser Tyr Arg Pro Ala Gln Gly Lys Val Leu Asn Ala			
258	660	665	670	
259	Arg Tyr Lys Tyr Gly Arg Asn Glu Lys Ile Tyr Leu Lys Ser Asp Gly			
260	675	680	685	
261	Ser Tyr Phe Tyr Asp Lys Leu Ser Gln Leu Asp Leu Ser Ala Gln Trp			
262	690	695	700	

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date